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Result
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Match
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AA935402 ch33h03.s
AW250048 Z819281.3
T61794 yb95e08.s1
A1973656 sd07h11.y
AZ760071 1M0553C03
AA232414 zr23b04.r
AA288258 vb17c12.r
                                                                                                              Description
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AUTHORS
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AL593945/c
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                                                                                                                                                                                                                                         mRNA sequence.
AL593945
AL593945.1 GI:
                                                                                                                                                                     Xenopodinae; Silurana.
1 (bases 1 to 59)
Huckle, E., Taylor, R.,
                                                                                                                                                                                              Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Mesobatrachia; Pipoidea; Pipidae;
                                                                                           Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TGas004c16.sp6
                                                                                                                             Contact: Huckle
Sanger Centre
                                                                                                                                              Sanger Xenopus tropicalis EST project 2001 Unpublished (2001)
                                                                                                                                                                                                                                   EST
                                                                                                                                                                                                                                                                  AL593945 XGC-gastrula
                                                                    This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
                                                                                    Sequencing primer:
                                                                                                                                                                                                                         western clawed frog.
                                                                                                                                                                                                                                                                                                                                              /organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="TGas004c16"
/clone_ib="XGC-gastrula"
/clone_ib="XGC-gastrula"
/dev_stage="gastrula (stages 10.5-13 mixed)"
/lab_host="Escherichia coli bH10B"
                                                           Location/Qualifiers
                                                     . 59
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Silurana tropicalis cDNA clone TGas004c16
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AA2454247
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BE317966
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AZ778327
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AB351796 NF066H05L
AW355214 pnf-b-p06
AZ778327 2M0013016
H28465 y055c05.s1
T70039 yc17b01.s1
A1959431 fd10a09.y
AL487252 T. brucei
AA754857 vu51e10.r
EF638275 NF044C09p
H55533 CHR220472 C
D67715 CELK076H4F
A1085127 oy15h02.s
W41103 mc39h12.r1
AA999944 ot02f08.s
BH011434 BG01842-5
AA142590 ms10b01.r
AA999542 TM0256C10
AA792062 vn69c06.r
AA77544 2330h04.x
N92878 zb71e08.s1
A1707742 as32h04.x
N92878 zb71e08.s1
A2813936 2M0081K20
B1082549 60287796
AZ316806 1M0035E13
AZ8316806 1M0035E13
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AI140952 qf24e01.x
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: kkorth@comp.uark.edu
Email: kkorth@comp Initiative accession:
Medicago Genome Initiative accession:
Insert Length: 659 Std Error: 0.00
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18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               University of Arkansas 217 Plant Science Building, Fayetteville, Tel: 501 575 5191 Fax: 501 575 7601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Korth K
Dept. of Plant Pathology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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BE322167
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                                                                                                                                                                                                                                                                                           expanded M. truncatula leaves of plants fed upon by Spodoptera exigua (beet armyworm) for 24 hours. Systemic (undamaged leaves from injured plants) and wounded leaves were harvested and pooled."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Insect herbivory"
/tissue_type="local and systemic leaves"
/dev_stage="mature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Medicago truncatula"
/db_xref="taxon:3880"
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Matches Query Match Best Local

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Conservative

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Score 14.6; DB 13 No. 3.7e+04;

DB 13;

Length 52; Indels

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BASE COUNT
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KEYWORDS
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DEFINITION
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AZ647203/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AZ647203 52 bp DNA
1M0513004R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0513004 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: CACACAGGAAACAGCTATGACC Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insert Length: 10000 Std En
Plate: 0513 row: O column:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and Wright, D., Weiss, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AZ647203.1 GI:11778434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria;
1 (bases 1 to 52)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               308,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             801 585 5606
801 585 7177
1: ddunn@genetics.utah.edu
                           21
                                                                                                                 Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA pollymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pND42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
     adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

13 c 8 g 10 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="C57BL/67"
/db_xref="taxon:10090"
/clone="UUGC1M0513004"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Weiss
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Rodentia;
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RESULT 5
AI920251/c
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AUTHORS
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                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                          1 ttattgtggccatctttgtccagc 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Gerald Rubin
Berkeley Drosophila Genome Project
University of California, Berkeley
LSA Building, Berkeley, CA 94720-3200,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQ025201 46 bp DNA GSS 23-AUG-2000 EP(3)1219 Drosophila melanogaster EP line Drosophila melanogaster genomic Sequence recovered from 5' end of P element, DNA sequence
                                   AI920251 55 bp mRNA EST 29-JUL-: 1781 Pine Lambda Zap Xylem library Pinus taeda cDNA clone
g5_PL21NCSU,
AI920251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Class: transposon-tagged.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: gerry@fruitfly.berkeley.edu
Sequence recovery method was inver:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liao, G.-C., Rehm, E.J. and Rubin, G.M.
Insertion site preferences of the P transposable element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                recognition sequence
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                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Drosophila melanogaster EP line"
/note="Inverse PCR was performed on Drosophila
melanogaster strains each of which contains a single EP
transposable element insertion. (The generation of these
insertion strains is described in Rorth P, Szabo K, Bailey
A, Laverty T, Rehm J, Rubin GM, Weigmann K, Milan M, Benes
V, Ansorge W, Cohen SM. 1998. Systematic gain-of-function
genetics in Drosophila. Development 6:1049-1057.) The
resultant fragment for each strain was directly sequenced
to determine the genomic sequence at the site of
insertion. Details of the protocols used can be found at
http://fruitfly.berkeley.edu/p_disrupt/inverse_pcr.html."
9 a 14 c 11 g 12 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                    mRNA sequence
                                                                                                                                                                                                                                                                             55.4%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sci. U.S.A. 97 (7), 3347-3351 (2000)
                                                                                                                                                                                                                                                         Score 14.4; DB 13;
Pred. No. 4.5e+04;
0; Mismatches 6;
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AA935402/c
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA935402 52 bp mRNA EST 28-APR-1998 oh33h03.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1459637 3 similar to SW:RL3_HUMAN P39023 60S RIBOSOMAL PROTEIN L3. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Forest Biotechnology Group
North Carolina State University
Dept. of Forestry, NC State University, 6113 Jordan Hall, Raleigh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pinus taeda
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trachec
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus;
                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D.,
Emmmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Stratagene, Inc. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Ross Whetten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Whetten, R.W., Kinlaw, C.S., Retzel, E. and Sederoff, R.R. The Pine Gene Discovery Project
                                                                                                                                                                                                                                         Tumor Gene Index
                                                                                                                                                                                                                                                                                      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: rosswhet@unity.ncsu.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
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                                                                                                                                                                                                                        Unpublished (1997)
                                                                                                                                                                                                                                                                  National Cancer Institute, Cancer
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919-515-7800
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/tissue_type="differentiating xylem"
/note="Vector: Lambda Zap; Site_1: EcoRI; Site_2: Xhol
Differentiating xylem was collected from the main stem
a 35-year old loblolly pine tree harvested during the
growing season. RNA isolation and library preparation
followed the methods of Allona et al., PNAS 95:9693-8,
1998"
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72.0%;
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                             information can
                                                    Sequencing Center
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TITLE
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Best Local :
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                                                                                                                                                                                 Contact: Robert Strainberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling

Tissue Procurement: DCTD/DTP cDNA Library Arrayed by: The I.M.A.G.E.

Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing

project Clone distribution: MGC clone distribution information can

be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality

Scores: PHRED from University of Washingtion Genome Center

Trimming: cross_match from University of Washingtion Genome Center

PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley

Drosophila Genome Project. University of Washingtion Genome Center:

http://www.genome.washington.edu Low Quality Sequence: 9 contiguous

PHRED high quality bases following vector sequence. Very Low

Quality Sequence: Trace file contained 29 contiguous distinct peaks

following vector sequence the prosecone
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                                                                                                                                                 following vector sequence. Polyadenylation: Based upon the presence of a xhoI site followed by a run of 14 or more T residues at the
                                                                                                                 Plate: LLCM1
                                                                                                                                 beginning of the sequence, this cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
Other_ESTs: 2819281.5prime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 29)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AW250048 29 bp mRNA ESI 7, J.T. 22819281.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819281 3',
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                                                                 quality sequence stop: 9.
Location/Qualifiers
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/db_xref="taxon:9606"
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/db_xref="taxon:9606"
/clone="IMAGE:1459637"
/clone_lib="NCI_CGAP_Kid6"
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77.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
Insert Size: 1721
High qality sequence stops: 1
High qality sequence starts: 1 High qality sequence stops: 1
Source: IMAGE Consortium, LLNL This clone is available royalty-fro
through LLNL; contact the IMAGE Consortium (info@image.linl.gov)
for further information. Trace considered overall poor quality
Insert Length: 1721 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hillier, L., Lennoń, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry, Meg, J., Trevaskis, E., Indexender (N.), Soares, M.B., Tan, F., Thierry, Meg, J., Trevaskis, E., Indexender (N.), Soares, M.B., Tan, F., Thierry, Meg, J., Trevaskis, E., Indexender (N.), Soares, M.B., Tan, F., Thierry, Meg, J., Trevaskis, E., Indexender (N.), Soares, M.B., Tan, F., Thierry, Meg, J., Trevaskis, E., Indexender (N.), Soares, M.B., Tan, F., Thierry, Meg, J., Trevaskis, E., Indexender (N.), Soares, M.B., Tan, F., Thierry, Meg, J., Trevaskis, E., Indexender (N.), Soares, M.B., Tan, F., Thierry, Meg, J., Trevaskis, E., Indexender (N.), Soares, M.B., Tan, F., Thierry, Meg, J., Trevaskis, E., Indexender (N.), Soares, M.B., Tan, F., Thierry, Meg, J., Trevaskis, E., Indexender (N.), Soares, M.B., Tan, F., Thierry, Meg, J., Trevaskis, E., Indexender (N.), Soares, M.B., Tan, F., Thierry, Meg, J., Trevaskis, E., Indexender (N.), Soares, M.B., Tan, F., Thierry, Meg, J., Trevaskis, E., Indexender (N.), Soares, M.B., Tan, F., Thierry, Meg, J., Trevaskis, E., Indexender (N.), Soares, M.B., Tan, F., Thierry, Meg, J., Trevaskis, E., Indexender (N.), Soares, M.B., Tan, F., Thierry, Meg, J., Thierry,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Underwood, K., Wöhldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 1.
• Location/Qualifiers
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Wilson RK
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yb95e08.s1 Stratagene liver (#937224) Homo sapiens cDNA clone
yMAGE:78950 3' similar to gb:K02403 COMPLEMENT C4 PRECURSOR (HUMAN
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                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="GDB:498695"
/db_xref="taxon:9606"
/clone="IMAGE:78950"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ECORI; CDNA made by oligo-dT priming. Directionally cloned into EcoRJXhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
/dev_stage="49 years old"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: liver; Vector: pBluescript SK; Site_1: EcoRI
                                                                                                                                          /sex="male"
                                                                                                                                                                         /clone_lib="Stratagene liver (#937224)"
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/tissue_type="small cell carcinoma"
/cell_line="MGC3"
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/cell_line="mous"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
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72.0%;
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Pred. No. 7.7e+04;
Pred. No. 7.7e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C. Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Dape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rossidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                               info@genomesystems.com web site: www.genomesystems.com
Trace considered overall poor quality
Seq primer: ~40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134 For further information call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314) 27-3324 or contact: clones@genomesystems.com or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
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                                                                                                                                                                                                                                                                     /organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1020-1054"
                                                                                                                                                                                                  /tissue_type="root nodules of greenhouse grown plants"
/lab_host="XL10-Gold"
performed with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stratagene's
                                                                                                                                                                           /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                         /clone_lib="Gm-c1020"
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9 ATGGTGCCCAACTTTATCAAACA attgtggccatctttgtccagca Matches

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       and phosphporylated. The XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size- fractionated with a 500 bp cutoff, using GibcoBRL Life Technologies' cDNA Size Predigested vector (pBluescript II SK+) that has been digested with EcoRI and XhoI, and phosphorylated by Stratagene. Both the white and blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (n=56) and sequence (n=16). This library was constructed by Dr. Paul Keim and Dr. Virginia Coryell."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            first-strand synthesis primer was used. An 'anchor' nucleotide (v=A, C, or G) was added to the 3' end of the primer [GAGAGAGAGAGAGAGAACTAGTCTGAG(T)18V] to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with cloned Pfu DNA polymerase and size- fractionated with a 400 bp cutoff, using a SizeSep 400 Spun column from the polymerase and size- fractionated with a 400 bp cutoff, using a SizeSep 400 Spun column from the polymerase and size- fractionated with a 400 bp cutoff, using a SizeSep 400 Spun column from the polymerase and size- fractionated with a 400 bp cutoff, using a SizeSep 400 Spun column from the polymerase and size- fractionated with a specific plant of the polymerase and size- fractionated with a specific plant of the polymerase and size- fractionated with a specific plant of the polymerase and size- fractionated with a specific plant of the polymerase and size- fractionated with a specific plant of the polymerase and size- fractionated with a specific plant of the polymerase and size- fractionated with a specific plant of the polymerase and size- fractionated with a specific plant of the polymerase and size- fractionated with a specific plant of the polymerase and size- fractionated with a specific plant of the polymerase and size- fractionated with a specific plant of the polymerase and size- fractionated with a specific plant of the polymerase and size- fractionated with a specific plant of the polymerase and size- fractionated with a specific plant of the polymerase and size- fractionated with a specific plant of the polymerase and size- fractionated with a specific plant of the polymerase and size- fractionated with a specific plant of the polymerase and size- fractionated with a specific plant of the polymerase and size- fractionated with a specific plant of the polymerase and size- fractionated with a specific plant of the polymerase and size- fractionated with a specific plant of the polymerase and size- fractionated with a speci
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51.5%;
73.9%;
Score 13.4; DB 10; Pred. No. 1.1e+05;
                                                                                         Length
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JOURNAL COMMENT REFERENCE AUTHORS SOURCE ORGANISM RESULT 1 AZ760071 FEATURES ACCESSION DEFINITION KEYWORDS /ERSION COCUS TITLE source 10 Dunn,D., Aoyagi,A., Barber,M., Beacorn,I., Duval,B., Human, I., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhaus High quality sequence stop: 33.
Location/Qualifiers Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: ( Plate: 0553 row: C column: 03 Seg primer: CACACAGGAAACAGCTATGACC and Wright, D., Weiss, R.
Mouse whole genome sca AZ760071 1M0553C03R Mouse 10kb plasmid UUGC1M Tel: 801 585 5606 Fax: 801 585 7177 University of Utah Genome Center University of Utah Unpublished (2000) Mus musculus AZ760071.1 clone UUGC1M0553C03 R, DNA sequence. AZ760071 Contact: Robert B. plasmid inserts Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus house mouse (bases 1 to 33) 308, USA plasmid ends Biomedical Polymers Research Bldg., /organism="Mus musculus" /strain="C57BL/6J" /db\_xref="taxon:10090" /clone="UUGC1M0553C03" /clone\_lib="Mouse 10kb plasmid UUGC1M library" GI:12867513 Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. 33 bp Weiss scaffolding with paired end reads from 10kb Std Error: 0.00 library Mus musculus Duval, B., Hamil, C., 20 S. 16-FEB-2001 2030 E., genomic SLC, UT

/lab\_host="E. Coli strain XL10-Gold,

T1-resistant,

/sex="Male"



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MEDLINE
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                                                                                                                                                                   Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry, Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                   Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA232414 46 bp mRNA EST 28-FEB-1997 zr23b04.rl Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:664207 5' similar to WP:K04G2.5 CE06099 ESTERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Wilson RK
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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AA232414.1 GI:1855201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pNA92 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
/clone_lib="Stratagene NT2 neuronal precursor 937230"
                              /db_xref="taxon:9606"
/clone="IMAGE:664207"
                                                                                       /organism="Homo sapiens"
/db_xref="GDB:5426137"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (http://www.jax.org/resources/documents/dnares/). The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory Mouse DNA Resource
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73.9%;
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SOURCE VERSION

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubgeisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B. Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                 WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMACE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The WashU-HHMI Mouse EST Project
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AA288258
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vb17c12.r1 Soares mouse 3NbMS Mus musculus
                                                                                                                                                                                                                                                                                                        Seq primer: -28m13 rev2 ET from Amersham.
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314 286 1810
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/tissue_type="Spleen"
/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="IMAGE:749206"
                                                                                                                                                                                                                                           /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                              /sex="male"
                                                                                                                                                                                             /clone_lib="Soares mouse 3NbMS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tissue_type="neuroepithelial cells"
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73.9%;
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Pred. No. 1.1e+05;
0; Mismatches 6
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three rounds of normalization, and was constructed by

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RESULT 14
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AA566958/c
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                                                                                                                     Qγ
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 BE317966 60 bp mRNA
NF060H05LF1F1044 Developing 1
NF060H05LF 5', mRNA sequence
                                                                                                                                               l Similarity 70.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Forest Biotechnology Group
North Carolina State University
Dept. of Forestry, NC State University, 6113 Jordan Hall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Allona, I., Quinn, M., Shoop, E., Swope, K., St.Cyr, S., Cai Riedl, J., Retzel, E., Campbell, M.M., Sederoff, R. and Whele Analysis of xylem formation in pine by cDNA sequencing Proc. Natl. Acad. Sci. U.S.A. 95 (16), 9693-9698 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: rosswhet@unity.ncsu.edu
Seq primer: T3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Ross Whetten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98356220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. 1 (bases 1 to 55)
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AA566958
AA566958.1 GI:3366171
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                                                                                                                                                                                                                          'note="Vector: lambda-ZAP; Site_1: EcoRI; Site_2: XhoI;
The library was made from immature xylem from the
underside of inclined stems of differentiating wood. A
mixture of four genotypes were used. Oligo-dT prime cDNA
was directionally cloned into the EcoRI-XhoI lambda-ZAP
vector arms" 15 g 12 t 2 others
                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:3352"
/clone="5c6g"
                                                                                                                                                                                                                                                                                                                                                                                   /organism="Pinus taeda"
/strain="Coastal plain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bento
                                                                                                                                                                                                                                                                                                                               /clone_lib="Loblolly pine
/tissue_type="Xylem"
                                                                                                                                                                                                                                                                                                                    /lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
                                                                                                                                                          51.5%;
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> C Pinus taeda cDNA clone 5c6g, mRNA sequence
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Pred. No. 1.2e
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7;
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              cDNA clone
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                                                                                                                                                                                                                                                                                                                               38
                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
Contact: Joan Burnside
Molecular Endocrinology
University of Delaware 40 Townsend Hall, Neway Tel: 302 831-1345
                                                                                                                                                       chicken.
Gallus gallus
                                                                          Burnside, J., Cogl
Chicken fat ESTs
                                                                                                                 Archosauria; Aves; N
Phasianinae; Gallus.
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barrel medic
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                                                                                         Cogburn, L.A.
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ACCESSION
VERSION
                                                                                   44 bp mRNA EST 07-MAY-2001 pnf-b.pk0001.a6 chicken fat cDNA library pBSII Gallus gallus cDNA clone pnf-b.pk0001.a6 5′ similar to (U76193) actin [Pisum sativum] gi|1724143 (U81049) actin [Pisum sativum], mRNA sequence.
AW355214
AW355214.1 GI:6857258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK 73402, Tel: 580 221 7381 Fax: 580 221 7380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Insert Length: 851 Std Error: 0.0 Plate: 060 row: H column: 05 Seg primer: TCACACAGGAAACAGCTATGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2000)
On Jul 14, 2000 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonza. Flores,H.R., Inman,J.T., Weller,J.W. and May,G. Expressed Sequence Tags from the Samuel Roberts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BE317966.2
                          Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Medicago truncatula leaf library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Medicago Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: gdmay@noble.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plant Biology Division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 60)
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="Pooled developmental"
/note="Vector: Lambda Zap; Contains a mixture of very
young, developing, mature and senescing leaves."
14 c 4 g 15 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Medicago truncatula"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Developing leaf"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                           51.5%;
93.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GI:11960762
                                                                                                                                                                                                                                                                                                                                   24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Initiative accession: 51 Std Error: 0.00
; Chordata; Craniata; Vertebrata; Neognathae; Galliformes; Phasian;
                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 13.4; DB 10
Pred. No. 1.2e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               replaced gi:9191743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGI:S:22065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gonzales, R.A., Bell, C.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               60;
                        Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Newark,

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Cogburn, L.A.

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BASE COUNT
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Search completed: March 9, 2002, 00:09:32 Job time: 11048 sec
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                                                                                                                 Ouery Match 50.8%; Score 13.2; DB 10; Length 44; Best Local Similarity 69.2%; Pred. No. 1.4e+05; Matches 18; Conservative 0; Mismatches 8; Indels (
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                                                                                                                 Gaps
                                                                                                                   0;
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